

APPLICANT FACSIMILE OF FORM PTO-1449 REV 7-80	U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTY DOCKET NO ENZ-004	SERIAL NO 10/032,827
LIST OF PUBLICATIONS CITED BY APPLICANT (Use several sheets if necessary)		APPLICANT Schwartz, John J. et al.	
		FILING DATE October 23, 2001	GROUP 3736

U.S. PATENT DOCUMENTS

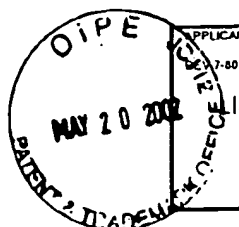
EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE IF APPROPRIATE
JD	A1	4,783,605	11/88	Tomisawa et al.	307	450	
	A2	5,190,873	03/93	Lernhardt et al.	435	177	
	A3	5,364,791	11/94	Vegeto et al.	435	320.1	
	A4	5,464,758	11/95	Gossen et al.	435	09.1	
	A5	5,834,266	11/98	Crabtree et al.	435	172.3	
	A6	5,874,534	02/99	Vegeto et al.	530	350	
	A7	5,882,924	03/99	Fritz et al.	435	320.1	
	A8	5,935,934	08/99	Vegeto et al.	514	44	
	A9	5,989,910	11/99	Mermod et al.	435	325	
	A10	6,069,239	05/00	Mathias	530	23.1	
V	A11	6,153,383	11/00	Verdine et al.	435	6	
JD	A12	6,157,872	12/00	Michael	700	247	

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	TRANSLATION	
							YES	NO
JD	A13	WO 93/23431 A1	11/93	PCT				
V	A14	WO 98/18925 A2,A3	05/98	PCT				
JD	A15	WO 99/42929 A1	08/99	PCT				

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JD	A16	Abouhamad et al. Computer-aided resolution of an experimental paradox in bacterial chemotaxis. <i>J. Bacteriol.</i> 1998 Aug;180(15):3757-64
	A17	Amara et al. A versatile synthetic dimerizer for the regulation of protein-protein interactions. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1997 Sep 30;94(20):10618-23
	A18	Appleby et al. Proposed signal transduction role for conserved CheY residue Thr87, a member of the response regulator active-site quintet. <i>J. Bacteriol.</i> 1998 Jul;180(14):3563-9
V	A19	Astromoff et al. A variant of λ repressor with an altered pattern of cooperative binding to DNA sites. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1995 Aug 29;92(18):8110-4
JD	A20	Baca et al. Phage display of a catalytic antibody to optimize affinity for transition-state analog binding. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1997 Sep 16;94(19):10063-8
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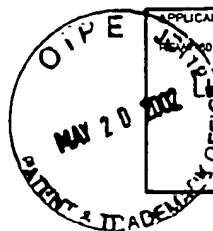
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JD	B1	Becskei et al. Engineering stability in gene networks by autoregulation. <i>Nature</i> 2000 Jun 1;405(6786):590-3
	B2	Belshaw et al. Controlling protein association and subcellular localization with a synthetic ligand that induces heterodimerization of proteins. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1996 May 14;93(10):4604-7
	B3	Bennett et al. Role of irreversibility in stabilizing complex and nonergodic behavior in locally interacting discrete systems. <i>Phys. Rev. Lett.</i> 1985 Aug 12;55(7):657-660
	B4	Bromberg et al. The role of STATs in transcriptional control and their impact on cellular function. <i>Oncogene</i> 2000 May 15;19(21):2468-73
	B5	Bass et al. Detection of a conserved α -helix in the kinase-docking region of the aspartate receptor by cysteine and disulfide scanning. <i>J. Biol. Chem.</i> 1998 Sep 25;273(39):25006-14
	B6	Beckett et al. Isolation of λ repressor mutants with defects in cooperative operator binding. <i>Biochemistry</i> 1993 Sep 7;32(35):9073-9
	B7	Bell et al. Crystal structure of the λ repressor C-terminal domain provides a model for cooperative operator binding. <i>Cell</i> 2000 Jun 23;101(7):801-11
	B8	Benson et al. Genetic selection for mutations that impair the co-operative binding of lambda repressor. <i>Mol. Microbiol.</i> 1994 Feb;11(3):567-79
	B9	Berlekamp et al. What's life. Winning Way for your Mathematical Plays, 2: Games in Particular. Chapter 25, pp. 817-850 (1982)
	B10	Beyersmann. Regulation of mammalian gene expression. In <i>New Approaches to Drug Development</i> (Jolles, P. ed.) pp. 9-28 (2000)
	B11	Bilwes et al. Structure of CheA, a signal-transducing histidine kinase. <i>Cell</i> 1999 Jan 8;96(1):131-41
	B12	Blat et al. Regulation of phosphatase activity in bacterial chemotaxis. <i>J. Mol. Biol.</i> 1998 Dec 11;284(4):1191-9
	B13	Bray et al. Computer analysis of the binding reactions leading to a transmembrane receptor-linked multiprotein complex involved in bacterial chemotaxis. <i>Mol. Biol. Cell.</i> 1995 Oct;6(10):1367-80
	B14	Burz et al. Single-site mutations in the C-terminal domain of bacteriophage λ cl repressor alter cooperative interactions between dimers adjacently bound to O_R . <i>Biochemistry.</i> 1994 Jul 19;33(28):8406-16
	B15	Bustos et al. Functional domains of the AraC protein. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1993 Jun 15;90(12):5836-42 Duplicate citation
	B16	Carey et al. An amino-terminal fragment of GAL4 binds DNA as a dimer. <i>J. Mol. Biol.</i> 1989 Oct 5;209(3):423-32
	B17	Carter et al. Endocytosis of functional epidermal growth factor receptor-green fluorescent protein chimera. <i>J. Biol. Chem.</i> 1998 Dec 25;273(52):35000-7
	B18	Culik et al. Computation theoretic aspects cellular automata. <i>Physica</i> 1990;45(1-3):357-378
	B19	Cohen et al. Modular binding domains in signal transduction proteins. <i>Cell</i> 1995 Jan 27;80(2):237-48
JD	B20	Da Re et al. Kinetics of CheY phosphorylation by small molecule phosphodonors. <i>FEBS Lett.</i> 1999 Sep 3;457(3):323-6
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JD	C1	Daugherty et al. Development of an optimized expression system for the screening of antibody libraries displayed on the <i>Escherichia coli</i> surface. <i>Protein Eng.</i> 1999 Jul;12(7):613-21
	C2	Djordjevic et al. Structural analysis of bacterial chemotaxis proteins: components of a dynamic signaling system. <i>J. Struct. Biol.</i> 1998 Dec 15;124(2-3):189-200
	C3	Donner et al. Carboxyl-terminal domain dimer interface mutant 434 repressors have altered dimerization and DNA binding specificities. <i>J. Mol. Biol.</i> 1998 Nov 13;283(5):931-46
	C4	Dove et al. Mechanism for a transcriptional activator that works at the isomerization step. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 2000 Nov 21;97(24):13215-20
	C5	Dove et al. Activation of prokaryotic transcription through arbitrary protein-protein contacts. <i>Nature</i> 1997 Apr 10;386(6625):627-30
	C6	Drexler. Molecular engineering: An approach to the development of general capabilities for molecular manipulation. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1981 September;78(9):5275-5278
	C7	Dutta et al. Histidine kinases: diversity of domain organization. <i>Mol. Microbiol.</i> 1999 Nov;34(4):633-40
	C8	Earhart et al. Use of an Lpp-OmpA fusion vehicle for bacterial surface display. <i>Methods Enzymol.</i> 2000;326:506-16
	C9	Eisenbach. Control of bacterial chemotaxis. <i>Mol. Microbiol.</i> 1996 Jun;20(5):903-10
	C10	Elowitz et al. A synthetic oscillatory network of transcriptional regulators. <i>Nature.</i> 2000 Jan 20;403(6767):335-8
	C11	Ermentrout et al. Cellular automata approaches to biological modeling. <i>J. Theor. Biol.</i> 1993 Jan 7;160(1):97-133
	C12	Finkelstein. Conservative logic. <i>Internat. J. Theor. Phys.</i> 1982;21(3/4):219-253
	C13	Firestine et al. Using an AraC-based three-hybrid system to detect biocatalysts in vivo. <i>Nat. Biotechnol.</i> 2000 May;18(5):544-7
	C14	Freiberg et al. Transcriptional control in keratinocytes and fibroblasts using synthetic ligands. <i>J. Clin. Invest.</i> 1997 Jun 1;99(11):2610-5
	C15	Frisch et al. Lattice-gas automata for the Navier-Stokes equation. <i>Phys. Rev. Lett.</i> 1986 Apr 7;56(14):1505-1508
	C16	Fuh et al. Analysis of PDZ domain-ligand interactions using carboxyl-terminal phage display. <i>J. Biol. Chem.</i> 2000 Jul 14;275(28):21486-91
	C17	Gardner. On cellular automata, self-reproduction, the garden of Eden and the game of "life." <i>Scientific American.</i> 1971;224(2):112-117
	C18	Gardner. The fantastic combinations of John Conway's new solitaire game "life." <i>Scientific American</i> 1970;223(4):120-123
	C19	Gardner et al. Construction of a genetic toggle switch in <i>Escherichia coli</i> . <i>Nature.</i> 2000 Jan 20;403(6767):339-42
↓	C20	Gether. Uncovering molecular mechanisms involved in activation of G protein-coupled receptors. <i>Endocr. Rev.</i> 2000 Feb;21(1):90-113
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JD	D1	Gilchrist et al. A dominant-negative strategy for studying roles of G proteins <i>in vivo</i> . <i>J. Biol. Chem.</i> 1999 Mar 5;274(10):6610-6
	D2	Gilchrist et al. Use of peptides-on-plasmids combinatorial library to identify high-affinity peptides that bind rhodopsin. <i>Methods Enzymol.</i> 2000;315:388-404
	D3	Gonzalez et al. An engineered allosteric switch in leucine-zipper oligomerization. <i>Nat. Struct. Biol.</i> 1996 Jun;3(6):510-5
	D4	Gouldson et al. Dimerization and domain swapping in G-protein-coupled receptors: a computational study. <i>Neuropsychopharmacology.</i> 2000 Oct;23(4 Suppl):S60-77
	D5	Guo et al. Designing small-molecule switches for protein-protein interactions. <i>Science.</i> 2000 Jun 16;288(5473):2042-5
	D6	New England Biolabs, Inc., GPS™-LS Linker Scanning System. <i>Technical Bulletin.</i> No. E7102, 2001;pp. 1-2
	D7	Hamm et al. Site of G protein binding to rhodopsin mapped with synthetic peptides from the α subunit. <i>Science.</i> 1988 Aug 12;241(4867):832-5
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	D9	Hamm. The many faces of G protein signaling. <i>J. Biol. Chem.</i> 1998 Jan 9;273(2):669-72.
	D10	Han et al. Peptides selected to bind the Gal80 repressor are potent transcriptional activation domains in yeast. <i>J. Biol. Chem.</i> 2000 May 19;275(20):14979-84
	D11	Hardy et al. Molecular dynamics of a classic lattice gas: transport properties and time correlations functions. <i>Physical Review A.</i> 1976 May;13(5):1949-1961
	D12	Harvey et al. Inducible control of gene expression: prospects for gene therapy. <i>Curr. Opin. Chem. Biol.</i> 1998 Aug;2(4):512-8
	D13	Hoogenboom et al. Natural and designer binding sites made by phage display technology. <i>Immunol Today.</i> 2000 Aug;21(8):371-8
	D14	Jasuja et al. Response tuning in bacterial chemotaxis. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1999 Sep 28;96(20):11346-51
	D15	Joung et al. A bacterial two-hybrid selection system for studying protein-DNA and protein-protein interactions. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 2000 Jun 20;97(13):7382-7
	D16	Kalkbrenner et al. Transcriptional activation by human <i>c-myb</i> and <i>v-myb</i> genes. <i>Oncogene.</i> 1990 May;5(5):657-61
	D17	Katz. Streptavidin-binding and -dimerizing ligands discovered by phage display, topochemistry, and structure-based design. <i>Biomol. Eng.</i> 1999 Dec 31;16(1-4):57-65
	D18	Kayman et al. The hypervariable domain of the murine leukemia virus surface protein tolerates large insertions and deletions, enabling development of a retroviral particle display system. <i>J. Virol.</i> 1999 Mar;73(3):1802-8
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JD	E1	Lee et al. Thyroid hormone receptor dimerization function maps to a conserved subregion of the ligand binding domain. <i>Mol. Endocrinol.</i> 1992 Nov;6(11):1867-73
	E2	Makeyev et al. Cell-free immunology: construction and in vitro expression of a PCR-based library encoding a single-chain antibody repertoire. <i>FEBS Lett.</i> 1999 Feb 12;444(2-3):177-80
	E3	Margolus. Physics-like models of computation. <i>Physica</i> 1984;10D:81-95
	E4	Marmorstein et al. DNA recognition by GAL4: structure of a protein-DNA complex. <i>Nature.</i> 1992 Apr 2;356(6368):408-14
	E5	Marshak et al. Synthetic peptide substrates for casein kinase II. <i>Methods Enzymol.</i> 1991;200:134-56
	E6	Marvin et al. Conversion of a maltose receptor into a zinc biosensor by computational design. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 2001 Apr 24;98(9):4955-60
	E7	McEvoy et al. Two binding modes reveal flexibility in kinase/response regulator interactions in the bacterial chemotaxis pathway. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1998 Jun 23;95(13):7333-8
	E8	Menon et al. Activation of <i>ara</i> operons by a truncated AraC protein does not require inducer. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1990 May;87(10):3708-12
	E9	Miyawaki et al. Dynamic and quantitative Ca ²⁺ measurements using improved cameleons. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1999 Mar 2;96(5):2135-40
	E10	Pabo et al. Geometric analysis and comparison of protein-DNA interfaces: why is there no simple code for recognition? <i>J. Mol. Biol.</i> 2000 Aug 18;301(3):597-624
	E11	Perrier et al. Toward a viable, self-reproducing universal computer. <i>Physica</i> 1996;D97 335
	E12	Roberts et al. RNA-peptide fusions for the <i>in vitro</i> selection of peptides and proteins. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1997 Nov 11;94(23):12297-302
	E13	Roychoudhury et al. Use of combinatorial library screening to identify inhibitors of a bacterial two-component signal transduction kinase. <i>Mol. Divers.</i> 1998;4(3):173-82
	E14	Saha et al. An operator-induced conformational change in the C-terminal domain of the λ repressor. <i>J. Biol. Chem.</i> 1992 Mar 25;267(9):5862-7
	E15	Schaffitzel et al. Ribosome display: an in vitro method for selection and evolution of antibodies from libraries. <i>J. Immunol. Methods.</i> 1999 Dec 10;231(1-2):119-35
	E16	Scharf et al. Control of direction of flagellar rotation in bacterial chemotaxis. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1998 Jan 6;95(1):201-6
	E17	Shimizu et al. Molecular model of a lattice of signalling proteins involved in bacterial chemotaxis. <i>Nat. Cell Biol.</i> 2000 Nov;2(11):792-6
	E18	Shukla et al. Mutations leading to altered CheA binding cluster on a face of CheY. <i>J. Biol. Chem.</i> 1995 Oct 13;270(41):24414-9
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JD	F1	Sipper. Non-uniform cellular automata: Evolution in rule space and formation of complex structures. In <i>Artificial Life IV</i> R. A. Brooks and P. Maes, eds, 1994;pps. 394-399, Cambridge, Massachusetts, The MIT Press.
	F2	Solà et al. Towards understanding a molecular switch mechanism: thermodynamic and crystallographic studies of the signal transduction protein CheY. <i>J. Mol. Biol.</i> 2000 Oct 20;303(2):213-25.
	F3	Swanson et al. Localized perturbations in CheY structure monitored by NMR identify a CheA binding interface. <i>Nat. Struct. Biol.</i> 1995 Oct;2(10):906-10
	F4	Takahashi et al. Measurement of intracellular calcium. <i>Physiol. Rev.</i> 1999 Oct;79(4):1089-125
	F5	Ten Dijke et al. Signaling inputs converge on nuclear effectors in TGF- β signaling. <i>Trends Biochem. Sci.</i> 2000 Feb;25(2):64-70
	F6	Toffoli. Cellular automata as an alternative to (rather than an approximation of) differential equations in modeling physics. <i>Physica</i> 1984;10D:117-127
	F7	Toffoli. Reversible computing. In <i>Lecture Notes in Computer Science</i> . J.W. Bakker and J. van Leeuwen, eds. 1980;pp. 632-644 Springer-Verlag, Berlin Heidelberg NY
	F8	Vichniac. Simulating physics with cellular automata. <i>Physica</i> 1984;10D: 96-116
	F9	Vichniac et al. Annealed and quenched inhomogeneous cellular automata (INCA). <i>J. Statistical Phys.</i> 1986;45(5-6):875-883
	F10	Welch et al. Structure of the CheY-binding domain of histidine kinase CheA in complex with CheY. <i>Nat. Struct. Biol.</i> 1998 Jan;5(1):25-9
	F11	Whaley et al. Selection of peptides with semiconductor binding specificity for directed nanocrystal assembly. <i>Nature</i> . 2000 Jun 8;405(6787):665-8
	F12	Whipple et al. Amino acid-amino acid contacts at the cooperativity interface of the bacteriophage λ and P22 repressors. <i>Genes Dev.</i> 1998 Sep 1;12(17):2791-802
	F13	Whipple et al. Specificity determinants for the interaction of λ repressor and P22 repressor dimers. <i>Genes Dev.</i> 1994 May 15;8(10):1212-23
	F14	Wolfe et al. Combining structure-based design with phage display to create new Cys ₂ His ₂ zinc finger dimers. <i>Structure</i> 2000 Jul 15;8(7):739-50
	F15	Wolfram. Cellular automata as models of complexity. <i>Nature</i> . 1984;311 419-424
	F16	Wolfram. Statistical mechanics of cellular automata. <i>Reviews of Modern Physics</i> . 1983;55(3):601-641
	F17	Wolfram. Universality and complexity in cellular automata. <i>Physica</i> 1984;10D(1&2):1-35
	F18	Xu et al. A bioluminescence resonance energy transfer (BRET) system application to interacting circadian clock proteins. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 1999 Jan 5;96(1):151-6
✓	F19	Zhang et al. Selection and application of peptide-binding peptides. <i>Nat. Biotechnol.</i> 2000 Jan;18(1):71-4
JD	F20	Zhu et al. Tyrosine 106 of CheY plays an important role in chemotaxis signal transduction in <i>Escherichia coli</i> . <i>J. Bacteriol.</i> 1996 Jul;178(14):4208-15
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